

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/037,657B
Source: 1FW16
Date Processed by STIC: 7/20/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/20/2006

PATENT APPLICATION: US/09/037,657B

TIME: 16:44:14

Input Set : A:\10857Z.SEQ.txt

Output Set: N:\CRF4\07202006\I037657B.raw

4 <110> APPLICANT: Hilton, Douglas J.
 5 Nicola, Nicos A.
 6 Farley, Alison
 7 Wilson, Tracy
 8 Zhang, Jian-Guo
 9 Alexander, Warren
 10 Rakar, Steven
 11 Fabri, Louis
 12 Kojima, Tetsuo
 13 Maeda, Masatsugu
 14 Kikuchi, Yasufumi
 15 Nash, Andrew
 17 <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
 18 ENCODING SAME
 20 <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
 22 <140> CURRENT APPLICATION NUMBER: 09/037,657B
 23 <141> CURRENT FILING DATE: 1998-03-10
 25 <150> PRIOR APPLICATION NUMBER: 08/928,720
 26 <151> PRIOR FILING DATE: 1997-09-11
 28 <160> NUMBER OF SEQ ID NOS: 58
 30 <170> SOFTWARE: PatentIn Ver. 2.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 5
 34 <212> TYPE: PRT
 35 <213> ORGANISM: Unknown
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Description of Unknown Organism: haemopoietin receptor
 40 <220> FEATURE:
 41 <221> NAME/KEY: UNSURE
 42 <222> LOCATION: (3)
 43 <223> OTHER INFORMATION: Unsure at position 3
 45 <400> SEQUENCE: 1
 W--> 46 Trp Ser Xaa Trp Ser
 47 1 5
 50 <210> SEQ ID NO: 2
 51 <211> LENGTH: 24
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Artificial Sequence
 55 <220> FEATURE:
 56 <223> OTHER INFORMATION: Description of Artificial Sequence: M116 probe
 59 <400> SEQUENCE: 2
 60 actcgctcca gattcccgcc tttt
 63 <210> SEQ ID NO: 3

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64 <211> LENGTH: 24
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Description of Artificial Sequence:M108 probe
71 <400> SEQUENCE: 3
72 tcccgcccttt ttgcacccat agat 24
75 <210> SEQ ID NO: 4
76 <211> LENGTH: 24
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Description of Artificial Sequence:M159 probe
83 <400> SEQUENCE: 4
84 ggtacttggc ttggaagagg aaat 24
87 <210> SEQ ID NO: 5
88 <211> LENGTH: 24
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence:M242 probe
95 <400> SEQUENCE: 5
96 cggctcacgt gcacgtcggg tggg 24
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 22
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence:M112 probe
107 <400> SEQUENCE: 6
108 agctgctgtt aaagggttc tc 22
111 <210> SEQ ID NO: 7
112 <211> LENGTH: 15
113 <212> TYPE: DNA
114 <213> ORGANISM: Unknown
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
120 <220> FEATURE:
121 <221> NAME/KEY: unsure
122 <222> LOCATION: (1)
123 <223> OTHER INFORMATION: Unsure at position 1
125 <220> FEATURE:
126 <221> NAME/KEY: unsure
127 <222> LOCATION: (7)
128 <223> OTHER INFORMATION: Unsure at position 7
130 <220> FEATURE:
131 <221> NAME/KEY: unsure
132 <222> LOCATION: (10)
133 <223> OTHER INFORMATION: Unsure at position 10

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135 <400> SEQUENCE: 7
136 rctccartcr ctcca 15
139 <210> SEQ ID NO: 8
140 <211> LENGTH: 15
141 <212> TYPE: DNA
142 <213> ORGANISM: Unknown
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
147 <220> FEATURE:
148 <221> NAME/KEY: unsure
149 <222> LOCATION: (1)
150 <223> OTHER INFORMATION: Unsure at position 1
152 <220> FEATURE:
153 <221> NAME/KEY: unsure
154 <222> LOCATION: (7)
155 <223> OTHER INFORMATION: Unsure at position 7
157 <220> FEATURE:
158 <221> NAME/KEY: unsure
159 <222> LOCATION: (10)
160 <223> OTHER INFORMATION: Unsure at position 10
162 <400> SEQUENCE: 8
163 rctccaytcr ctcca 15
166 <210> SEQ ID NO: 9
167 <211> LENGTH: 21
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Artificial Sequence:1944 probe
174 <400> SEQUENCE: 9
175 aagtgtgacc atcatgtgga c 21
178 <210> SEQ ID NO: 10
179 <211> LENGTH: 18
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence:2106 probe
186 <400> SEQUENCE: 10
187 ggaggtgtta aggaggcg 18
190 <210> SEQ ID NO: 11
191 <211> LENGTH: 18
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Description of Artificial Sequence:2120 probe
198 <400> SEQUENCE: 11
199 atgcccgcgg gtcgcccg 18
202 <210> SEQ ID NO: 12
203 <211> LENGTH: 1629
204 <212> TYPE: DNA

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205 <213> ORGANISM: Unknown
207 <220> FEATURE:
208 <221> NAME/KEY: CDS
209 <222> LOCATION: (124)..(1362)
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1
214 <400> SEQUENCE: 12
215 ggcacgagct tcgctgtccg cgcccgagtga cgcgcggtgcg gacccgagcc ccaatctgca 60
217 ccccgagac tcgccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120
219 ccc atg ccc gcg ggt cgc ccg gcc ccc gtc gcc caa tcc gcg cgg cgg 168
220 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
221 1 5 10 15
223 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216
224 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
225 20 25 30
227 ctc ggg gtg cct cgg gcc gga tcg gga gcc cac aca gct gta atc agc 264
228 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
229 35 40 45
231 ccc cag gac ccc acc ctt ctc atc gcc tcc tcc ctg caa gct acc tgc 312
232 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
233 50 55 60
235 tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
236 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
237 65 70 75
239 acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 408
240 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
241 80 85 90 95
243 acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
244 Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
245 100 105 110
247 cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
248 Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
249 115 120 125
251 gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
252 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
253 130 135 140
255 atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca 600
256 Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
257 145 150 155
259 ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag 648
260 Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
261 160 165 170 175
263 tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac 696
264 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
265 180 185 190
267 act gtg gcc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc 744
268 Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
269 195 200 205
271 act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca 792

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272 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
273      210      215      220
275 aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac 840
276 Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
277      225      230      235
279 ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag 888
280 Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
281 240      245      250      255
283 ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc 936
284 Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
285      260      265      270
287 caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg 984
288 Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
289      275      280      285
291 aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc 1032
293 Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
294      290      295      300
296 ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc 1080
297 Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
298      305      310      315
300 ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac 1128
301 Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
302 320      325      330      335
304 ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc 1176
305 Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
306      340      345      350
308 ggg gtg tgc gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg 1224
309 Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
310      355      360      365
312 cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc 1272
313 Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
314      370      375      380
316 tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag 1320
317 Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
318      385      390      395
320 aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc 1362
321 Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
322 400      405      410
324 taaggatagg ccattctcct gctgggtcag acctggaggc tcacctgaat tggagcccct 1422
326 ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa 1482
328 ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaagggttg 1542
330 ggtattgcag ggctcccaa caatctcttt aaataaataa aggagttgtt caggtaaaaa 1602
332 aaaaaaaaaa aaaaaaaaaa aaaaaaa 1629
335 <210> SEQ ID NO: 13
336 <211> LENGTH: 413
337 <212> TYPE: PRT
338 <213> ORGANISM: Unknown
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/037,657B

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3
Seq#:29; Xaa Pos. 136,139,162,177

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:21; Line(s) 949

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:45